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SEQUENCE LISTING

<110> SIMMONS, ANTHONY
CHEN, JIANMIN

<120> COMPOSITIONS AND METHODS FOR HERPES SIMPLEX PROPHYLAXIS
AND TREATMENT

<130> UTFG:263WO

<140> UNKNOWN

<141> 2004-07-26

<150> 60/489,984

<151> 2003-07-23

<160> 36

<170> PatentIn Ver. 2.1

<210> 1

<211> 921

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 1

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gacatccaga tgaccagtc tccatcctcc ttatctgcct ctctgggaga aagagtcagt 180
ctcaacttgtc gggcaagtca ggaaattagt gcttacttaa gctggcttca gcagaaacca 240
gatggaacta ttaaagcct gatctacgcc gcatccactt tagattctgg tgtcccaaaa 300
aggttcagtg gcagtaggtc tgggtcagat tattctctca ccatcagcag ccttgagtct 360
gaagattttg cagactatta ctgtctacaa tatgctagtt atccgctcac gttcgggtgt 420
gggaccaagc tggagctggg cgggtggcga tcgggtggag gaggcagcgg aggcgggtgg 480
tcggtgaagc tgcaggagtc tggacctgag ctggtgaagc ctggggcttc agtgaagatg 540
tcctgcaagg cttctggcta caccttcaca agctcctatg tacactgggt gaagcagagg 600
cctggacagg gacttgagtg gattggatgg atttatcctg gacatagtag tactaagtac 660
aatgagaagt tcatgggcaa gaccatattg actgcggaca aatcctccag cacagcctac 720
atgttgctca gcagcctgac ctctgaggac tctgcgatat atttctgtac aaggcaggag 780
gtacgactct ggtacttcga tgtctggggc gcagggacca cggtcaccgt ctccgcggcc 840
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catcatcatc atcatcattg a 921
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<211> 306

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
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Gly Ser Thr Gly Asp Ala Ala Gln Pro Ala Arg Arg Ala Arg Arg Thr
20 25 30
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Lys Leu Gly Thr Glu Leu Gly Ser Asp Ile Gln Met Thr Gln Ser Pro
 35 40 45
 Ser Ser Leu Ser Ala Ser Leu Gly Glu Arg Val Ser Leu Thr Cys Arg
 50 55 60
 Ala Ser Gln Glu Ile Ser Ala Tyr Leu Ser Trp Leu Gln Gln Lys Pro
 65 70 75 80
 Asp Gly Thr Ile Lys Arg Leu Ile Tyr Ala Ala Ser Thr Leu Asp Ser
 85 90 95
 Gly Val Pro Lys Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser
 100 105 110
 Leu Thr Ile Ser Ser Leu Glu Ser Glu Asp Phe Ala Asp Tyr Tyr Cys
 115 120 125
 Leu Gln Tyr Ala Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu
 130 135 140
 Glu Leu Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 145 150 155 160
 Ser Val Lys Leu Gln Glu Ser Gly Pro Glu Leu Val Lys Pro Gly Ala
 165 170 175
 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Ser
 180 185 190
 Tyr Val His Trp Val Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile
 195 200 205
 Gly Trp Ile Tyr Pro Gly His Ser Ser Thr Lys Tyr Asn Glu Lys Phe
 210 215 220
 Met Gly Lys Thr Ile Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
 225 230 235 240
 Met Leu Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Ile Tyr Phe Cys
 245 250 255
 Thr Arg Gln Glu Val Arg Leu Trp Tyr Phe Asp Val Trp Gly Ala Gly
 260 265 270
 Thr Thr Val Thr Val Ser Ala Ala Ala Arg Gly Gly Pro Glu Gln Lys
 275 280 285
 Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp His His His His
 290 295 300
 His His
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<210> 3
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 <212> DNA
 <213> Artificial Sequence

<220>
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Primer

<400> 3
tggtgggaag atggatacag 20

<210> 4
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<400> 4
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<210> 5
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<212> DNA
<213> Artificial Sequence

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<210> 6
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<212> DNA
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<223> Description of Artificial Sequence: Synthetic
Primer

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ggtgatatcg tkctcacysa rtctccagca at 32

<210> 7
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<212> DNA
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<400> 7
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<210> 8
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<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
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<400> 8
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<210> 9
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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Primer

<400> 9
tcagcttcyt gctaatacagt g 21

<210> 10
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<220>
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<400> 10
tgggtatctg gtrcstgtg 19

<210> 11
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<213> Artificial Sequence

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Primer

<400> 11
gtttcmaggt rccagatgt 19

<210> 12
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 12
tgttttcaag gtrccagatg t 21

<210> 13
<211> 20
<212> DNA
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Primer

<400> 13
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<210> 14
<211> 18
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Primer

<400> 14
tgctkckctg ggttcag 18

<210> 15
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Primer

<400> 15
taacccttga ccaggcatcc 20

<210> 16
<211> 36
<212> DNA
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Primer

<400> 16
gaggtgaagc tgcaggagtc aggacctagc ctggtg 36

<210> 17
<211> 22
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 17
aggtvmaact gcagvagtcw gg 22

<210> 18
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 18
aggtvvagct gcagvagtcw gg 22

<210> 19
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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Primer

<400> 19
actgcaggtr tccactcc 18

<210> 20
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 20
rctacaggtg tccactcc 18

<210> 21
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
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Primer

<400> 21
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<210> 22
<211> 18
<212> DNA
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<220>
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Primer

<400> 22
actgcaggtg tcctctct 18

<210> 23
<211> 18
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 23
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<210> 24
<211> 18
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 24
ccaagctgtg tcctrtcc 18

<210> 25
<211> 18
<212> DNA
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<223> Description of Artificial Sequence: Synthetic
Primer

<400> 25
ccaagctgtg tcctrtcc 18

<210> 26
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 26
tggtgacagy cvttcckggt 20

<210> 27
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 27
taytttaaaa rgtgtcmagt gt 22

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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Primer

<400> 28
ctyttaaaaag gkggtccagwg 20

<210> 29
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
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Primer

<400> 29
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<210> 30
<211> 17
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 30
atggcagcwg cycaaag 17

<210> 31
<211> 21
<212> DNA
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<220>
<223> Description of Artificial Sequence: Synthetic
Primer

<400> 31
ctttttaaaag wtgtccagkg t 21

<210> 32
<211> 19
<212> DNA
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<220>
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Primer

<400> 32

cttcctgatg gcagtggtt

19

<210> 33

<211> 904

<212> PRT

<213> human herpesvirus 1

<400> 33

Met Arg Gln Gly Ala Pro Ala Arg Gly Arg Arg Trp Phe Val Val Trp
 1 5 10 15

Ala Leu Leu Gly Leu Thr Leu Gly Val Leu Val Ala Ser Ala Ala Pro
 20 25 30

Ser Ser Pro Gly Thr Pro Gly Val Ala Ala Ala Thr Gln Ala Ala Asn
 35 40 45

Gly Gly Pro Ala Thr Pro Ala Pro Pro Ala Pro Gly Ala Pro Pro Thr
 50 55 60

Gly Asp Pro Lys Pro Lys Lys Asn Arg Lys Pro Lys Pro Pro Lys Pro
 65 70 75 80

Pro Arg Pro Ala Gly Asp Asn Ala Thr Val Ala Ala Gly His Ala Thr
 85 90 95

Leu Arg Glu His Leu Arg Asp Ile Lys Ala Glu Asn Thr Asp Ala Asn
 100 105 110

Phe Tyr Val Cys Pro Pro Pro Thr Gly Ala Thr Val Val Gln Phe Glu
 115 120 125

Gln Pro Arg Arg Cys Pro Thr Arg Pro Glu Gly Gln Asn Tyr Thr Glu
 130 135 140

Gly Ile Ala Val Val Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys
 145 150 155 160

Ala Thr Met Tyr Tyr Lys Asp Val Thr Val Ser Gln Val Trp Phe Gly
 165 170 175

His Arg Tyr Ser Gln Phe Met Gly Ile Phe Glu Asp Arg Ala Pro Val
 180 185 190

Pro Phe Glu Glu Val Ile Asp Lys Ile Asn Ala Lys Gly Val Cys Arg
 195 200 205

Ser Thr Ala Lys Tyr Val Arg Asn Asn Leu Glu Thr Thr Ala Phe His
 210 215 220

Arg Asp Asp His Glu Thr Asp Met Glu Leu Lys Pro Ala Asn Ala Ala
 225 230 235 240

Thr Arg Thr Ser Arg Gly Trp His Thr Thr Asp Leu Lys Tyr Asn Pro
 245 250 255

Ser Arg Val Glu Ala Phe His Arg Tyr Gly Thr Thr Val Asn Cys Ile
 260 265 270

Val Glu Glu Val Asp Ala Arg Ser Val Tyr Pro Tyr Asp Glu Phe Val
 275 280 285

Leu Ala Thr Gly Asp Phe Val Tyr Met Ser Pro Phe Tyr Gly Tyr Arg
 290 295 300
 Glu Gly Ser His Thr Glu His Thr Ser Tyr Ala Ala Asp Arg Phe Lys
 305 310 315 320
 Gln Val Asp Gly Phe Tyr Ala Arg Asp Leu Thr Thr Lys Ala Arg Ala
 325 330 335
 Thr Ala Pro Thr Thr Arg Asn Leu Leu Thr Thr Pro Lys Phe Thr Val
 340 345 350
 Ala Trp Asp Trp Val Pro Lys Arg Pro Ser Val Cys Thr Met Thr Lys
 355 360 365
 Trp Gln Glu Val Asp Glu Met Leu Arg Ser Glu Tyr Gly Gly Ser Phe
 370 375 380
 Arg Phe Ser Ser Asp Ala Ile Ser Thr Thr Phe Thr Thr Asn Leu Thr
 385 390 395 400
 Glu Tyr Pro Leu Ser Arg Val Asp Leu Gly Asp Cys Ile Gly Lys Asp
 405 410 415
 Ala Arg Asp Ala Met Asp Arg Ile Phe Ala Arg Arg Tyr Asn Ala Thr
 420 425 430
 His Ile Lys Val Gly Gln Pro Gln Tyr Tyr Leu Ala Asn Gly Gly Phe
 435 440 445
 Leu Ile Ala Tyr Gln Pro Leu Leu Ser Asn Thr Leu Ala Glu Leu Tyr
 450 455 460
 Val Arg Glu His Leu Arg Glu Gln Ser Arg Lys Pro Pro Asn Pro Thr
 465 470 475 480
 Pro Pro Pro Pro Gly Ala Ser Ala Asn Ala Ser Val Glu Arg Ile Lys
 485 490 495
 Thr Thr Ser Ser Ile Glu Phe Ala Arg Leu Gln Phe Thr Tyr Asn His
 500 505 510
 Ile Gln Arg His Val Asn Asp Met Leu Gly Arg Val Ala Ile Ala Trp
 515 520 525
 Cys Glu Leu Gln Asn His Glu Leu Thr Leu Trp Asn Glu Ala Arg Lys
 530 535 540
 Leu Asn Pro Asn Ala Ile Ala Ser Ala Thr Val Gly Arg Arg Val Ser
 545 550 555 560
 Ala Arg Met Leu Gly Asp Val Met Ala Val Ser Thr Cys Val Pro Val
 565 570 575
 Ala Ala Asp Asn Val Ile Val Gln Asn Ser Met Arg Ile Ser Ser Arg
 580 585 590
 Pro Gly Ala Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg Tyr Glu Asp
 595 600 605
 Gln Gly Pro Leu Val Glu Gly Gln Leu Gly Glu Asn Asn Glu Leu Arg
 610 615 620

Leu Thr Arg Asp Ala Ile Glu Pro Cys Thr Val Gly His Arg Arg Tyr
625 630 635 640

Phe Thr Phe Gly Gly Gly Tyr Val Tyr Phe Glu Glu Tyr Ala Tyr Ser
645 650 655

His Gln Leu Ser Arg Ala Asp Ile Thr Thr Val Ser Thr Phe Ile Asp
660 665 670

Leu Asn Ile Thr Met Leu Glu Asp His Glu Phe Val Pro Leu Glu Val
675 680 685

Tyr Thr Arg His Glu Ile Lys Asp Ser Gly Leu Leu Asp Tyr Thr Glu
690 695 700

Val Gln Arg Arg Asn Gln Leu His Asp Leu Arg Phe Ala Asp Ile Asp
705 710 715 720

Thr Val Ile His Ala Asp Ala Asn Ala Ala Met Phe Ala Gly Leu Gly
725 730 735

Ala Phe Phe Glu Gly Met Gly Asp Leu Gly Arg Ala Val Gly Lys Val
740 745 750

Val Met Gly Ile Val Gly Gly Val Val Ser Ala Val Ser Gly Val Ser
755 760 765

Ser Phe Met Ser Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val
770 775 780

Leu Ala Gly Leu Ala Ala Ala Phe Phe Ala Phe Arg Tyr Val Met Arg
785 790 795 800

Leu Gln Ser Asn Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Glu
805 810 815

Leu Lys Asn Pro Thr Asn Pro Asp Ala Ser Gly Glu Gly Glu Glu Gly
820 825 830

Gly Asp Phe Asp Glu Ala Lys Leu Ala Glu Ala Arg Glu Met Ile Arg
835 840 845

Tyr Met Ala Leu Val Ser Ala Met Glu Arg Thr Glu His Lys Ala Lys
850 855 860

Lys Lys Gly Thr Ser Ala Leu Leu Ser Ala Lys Val Thr Asp Met Val
865 870 875 880

Met Arg Lys Arg Arg Asn Thr Asn Tyr Thr Gln Val Pro Asn Lys Asp
885 890 895

Gly Asp Ala Asp Glu Asp Asp Leu
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<210> 34

<211> 904

<212> PRT

<213> human herpesvirus 2

<400> 34

Met Arg Gly Gly Gly Leu Ile Cys Ala Leu Val Val Gly Ala Leu Val

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Ser Gly Gly Val Ala Ala Thr Val Ala Ala Asn Gly Gly Pro Ala Ser	35	40	45
Arg Pro Pro Pro Val Pro Ser Pro Ala Thr Thr Lys Ala Arg Lys Arg	50	55	60
Lys Thr Lys Lys Pro Pro Lys Arg Pro Glu Ala Thr Pro Pro Pro Asp	65	70	75
Ala Asn Ala Thr Val Ala Ala Gly His Ala Thr Leu Arg Ala His Leu	85	90	95
Arg Glu Ile Lys Val Glu Asn Ala Asp Ala Gln Phe Tyr Val Cys Pro	100	105	110
Pro Pro Thr Gly Ala Thr Val Val Gln Phe Glu Gln Pro Arg Arg Cys	115	120	125
Pro Thr Arg Pro Glu Gly Gln Asn Tyr Thr Glu Gly Ile Ala Val Val	130	135	140
Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys Ala Thr Met Tyr Tyr	145	150	155
Lys Asp Val Thr Val Ser Gln Val Trp Phe Gly His Arg Tyr Ser Gln	165	170	175
Phe Met Gly Ile Phe Glu Asp Arg Ala Pro Val Pro Phe Glu Glu Val	180	185	190
Ile Asp Lys Ile Asn Thr Lys Gly Val Cys Arg Ser Thr Ala Lys Tyr	195	200	205
Val Arg Asn Asn Met Glu Thr Thr Ala Phe His Arg Asp Asp His Glu	210	215	220
Thr Asp Met Glu Leu Lys Pro Ala Lys Val Ala Thr Arg Thr Ser Arg	225	230	235
Gly Trp His Thr Thr Asp Leu Lys Tyr Asn Pro Ser Arg Val Glu Ala	245	250	255
Phe His Arg Tyr Gly Thr Thr Val Asn Cys Ile Val Glu Glu Val Asp	260	265	270
Ala Arg Ser Val Tyr Pro Tyr Asp Glu Phe Val Leu Ala Thr Gly Asp	275	280	285
Phe Val Tyr Met Ser Pro Phe Tyr Gly Tyr Arg Glu Gly Ser His Thr	290	295	300
Glu His Thr Ser Tyr Ala Ala Asp Arg Phe Lys Gln Val Asp Gly Phe	305	310	315
Tyr Ala Arg Asp Leu Thr Thr Lys Ala Arg Ala Thr Ser Pro Thr Thr	325	330	335
Arg Asn Leu Leu Thr Thr Pro Lys Phe Thr Val Ala Trp Asp Trp Val			

340					345					350					
Pro	Lys	Arg	Pro	Ala	Val	Cys	Thr	Met	Thr	Lys	Trp	Gln	Glu	Val	Asp
		355						360					365		
Glu	Met	Leu	Arg	Ala	Glu	Tyr	Gly	Gly	Ser	Phe	Arg	Phe	Ser	Ser	Asp
	370					375					380				
Ala	Ile	Ser	Thr	Thr	Phe	Thr	Thr	Asn	Leu	Thr	Glu	Tyr	Ser	Leu	Ser
385					390					395					400
Arg	Val	Asp	Leu	Gly	Asp	Cys	Ile	Gly	Arg	Asp	Ala	Arg	Glu	Ala	Ile
				405					410					415	
Asp	Arg	Met	Phe	Ala	Arg	Lys	Tyr	Asn	Ala	Thr	His	Ile	Lys	Val	Gly
		420						425					430		
Gln	Pro	Gln	Tyr	Tyr	Leu	Ala	Thr	Gly	Gly	Phe	Leu	Ile	Ala	Tyr	Gln
		435					440					445			
Pro	Leu	Leu	Ser	Asn	Thr	Leu	Ala	Glu	Leu	Tyr	Val	Arg	Glu	Tyr	Met
	450					455					460				
Arg	Glu	Gln	Asp	Arg	Lys	Pro	Arg	Asn	Ala	Thr	Pro	Ala	Pro	Leu	Arg
465					470					475					480
Glu	Ala	Pro	Ser	Ala	Asn	Ala	Ser	Val	Glu	Arg	Ile	Lys	Thr	Thr	Ser
				485					490					495	
Ser	Ile	Glu	Phe	Ala	Arg	Leu	Gln	Phe	Thr	Tyr	Asn	His	Ile	Gln	Arg
		500						505					510		
His	Val	Asn	Asp	Met	Leu	Gly	Arg	Ile	Ala	Val	Ala	Trp	Cys	Glu	Leu
		515					520					525			
Gln	Asn	His	Glu	Leu	Thr	Leu	Trp	Asn	Glu	Ala	Arg	Lys	Leu	Asn	Pro
	530					535					540				
Asn	Ala	Ile	Ala	Ser	Ala	Thr	Val	Gly	Arg	Arg	Val	Ser	Ala	Arg	Met
545					550					555					560
Leu	Gly	Asp	Val	Met	Ala	Val	Ser	Thr	Cys	Val	Pro	Val	Ala	Pro	Asp
				565					570				575		
Asn	Val	Ile	Val	Gln	Asn	Ser	Met	Arg	Val	Ser	Ser	Arg	Pro	Gly	Thr
		580						585					590		
Cys	Tyr	Ser	Arg	Pro	Leu	Val	Ser	Phe	Arg	Tyr	Glu	Asp	Gln	Gly	Pro
		595					600					605			
Leu	Ile	Glu	Gly	Gln	Leu	Gly	Glu	Asn	Asn	Glu	Leu	Arg	Leu	Thr	Arg
	610					615					620				
Asp	Ala	Leu	Glu	Pro	Cys	Thr	Val	Gly	His	Arg	Arg	Tyr	Phe	Ile	Phe
625					630					635					640
Gly	Gly	Gly	Tyr	Val	Tyr	Phe	Glu	Glu	Tyr	Ala	Tyr	Ser	His	Gln	Leu
				645					650					655	
Ser	Arg	Ala	Asp	Val	Thr	Thr	Val	Ser	Thr	Phe	Ile	Asp	Leu	Asn	Ile
		660						665				670			
Thr	Met	Leu	Glu	Asp	His	Glu	Phe	Val	Pro	Leu	Glu	Val	Tyr	Thr	Arg

675 680 685
 His Glu Ile Lys Asp Ser Gly Leu Leu Asp Tyr Thr Glu Val Gln Arg
 690 695 700
 Arg Asn Gln Leu His Asp Leu Arg Phe Ala Asp Ile Asp Thr Val Ile
 705 710 715 720
 Arg Ala Asp Ala Asn Ala Ala Met Phe Ala Gly Leu Cys Ala Phe Phe
 725 730 735
 Glu Gly Met Gly Asp Leu Gly Arg Ala Val Gly Lys Val Val Met Gly
 740 745 750
 Val Val Gly Gly Val Val Ser Ala Val Ser Gly Val Ser Ser Phe Met
 755 760 765
 Ser Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu Val Leu Ala Gly
 770 775 780
 Leu Val Ala Ala Phe Phe Ala Phe Arg Tyr Val Leu Gln Leu Gln Arg
 785 790 795 800
 Asn Pro Met Lys Ala Leu Tyr Pro Leu Thr Thr Lys Glu Leu Lys Thr
 805 810 815
 Ser Asp Pro Gly Gly Val Gly Gly Glu Gly Glu Glu Gly Ala Glu Gly
 820 825 830
 Gly Gly Phe Asp Glu Ala Lys Leu Ala Glu Ala Arg Glu Met Ile Arg
 835 840 845
 Tyr Met Ala Leu Val Ser Ala Met Glu Arg Thr Glu His Lys Ala Arg
 850 855 860
 Lys Lys Gly Thr Ser Ala Leu Leu Ser Ser Lys Val Thr Asn Met Val
 865 870 875 880
 Leu Arg Lys Arg Asn Lys Ala Arg Tyr Ser Pro Leu His Asn Glu Asp
 885 890 895
 Glu Ala Gly Asp Glu Asp Glu Leu
 900

<210> 35

<211> 394

<212> PRT

<213> human herpesvirus 1

<400> 35

Met Gly Gly Ala Ala Ala Arg Leu Gly Ala Val Ile Leu Phe Val Val
 1 5 10 15

Ile Val Gly Leu His Gly Val Arg Ser Lys Tyr Ala Leu Val Asp Ala
 20 25 30

Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asp Leu Pro
 35 40 45

Val Leu Asp Gln Leu Thr Asp Pro Pro Gly Val Arg Arg Val Tyr His
 50 55 60

Ile Gln Ala Gly Leu Pro Asp Pro Phe Gln Pro Pro Ser Leu Pro Ile
 65 70 75 80
 Thr Val Tyr Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu
 85 90 95
 Asn Ala Pro Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Glu Asp
 100 105 110
 Val Arg Lys Gln Pro Tyr Asn Leu Thr Ile Ala Trp Phe Arg Met Gly
 115 120 125
 Gly Asn Cys Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Ser
 130 135 140
 Tyr Asn Lys Ser Leu Gly Ala Cys Pro Ile Arg Thr Gln Pro Arg Trp
 145 150 155 160
 Asn Tyr Tyr Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe
 165 170 175
 Leu Met His Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu
 180 185 190
 Val Lys Ile Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His
 195 200 205
 Arg Ala Lys Gly Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro
 210 215 220
 Ser Ala Cys Leu Ser Pro Gln Ala Tyr Gln Gln Gly Val Thr Val Asp
 225 230 235 240
 Ser Ile Gly Met Leu Pro Arg Phe Ile Pro Glu Asn Gln Arg Thr Val
 245 250 255
 Ala Val Tyr Ser Leu Lys Ile Ala Gly Trp His Gly Pro Lys Ala Pro
 260 265 270
 Tyr Thr Ser Thr Leu Leu Pro Pro Glu Leu Ser Glu Thr Pro Asn Ala
 275 280 285
 Thr Gln Pro Glu Leu Ala Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu
 290 295 300
 Glu Asp Pro Val Gly Thr Val Ala Pro Gln Ile Pro Pro Asn Trp His
 305 310 315 320
 Ile Pro Ser Ile Gln Asp Ala Ala Thr Pro Tyr His Pro Pro Ala Thr
 325 330 335
 Pro Asn Asn Met Gly Leu Ile Ala Gly Ala Val Gly Gly Ser Leu Leu
 340 345 350
 Ala Ala Leu Val Ile Cys Gly Ile Val Tyr Trp Met Arg Arg His Thr
 355 360 365
 Gln Lys Ala Pro Lys Arg Ile Arg Leu Pro His Ile Arg Glu Asp Asp
 370 375 380
 Gln Pro Ser Ser His Gln Pro Leu Phe Tyr
 385 390

<210> 36

<211> 393

<212> PRT

<213> human herpesvirus 2

<400> 36

Met Gly Arg Leu Thr Ser Gly Val Gly Thr Ala Ala Leu Leu Val Val
 1 5 10 15

Ala Val Gly Leu Arg Val Val Cys Ala Lys Tyr Ala Leu Ala Asp Pro
 20 25 30

Ser Leu Lys Met Ala Asp Pro Asn Arg Phe Arg Gly Lys Asn Leu Pro
 35 40 45

Val Leu Asp Gln Leu Thr Asp Pro Pro Gly Val Lys Arg Val Tyr His
 50 55 60

Ile Gln Pro Ser Leu Glu Asp Pro Phe Gln Pro Pro Ser Ile Pro Ile
 65 70 75 80

Thr Val Tyr Tyr Ala Val Leu Glu Arg Ala Cys Arg Ser Val Leu Leu
 85 90 95

His Ala Pro Ser Glu Ala Pro Gln Ile Val Arg Gly Ala Ser Asp Glu
 100 105 110

Ala Arg Lys His Thr Tyr Asn Leu Thr Ile Ala Trp Tyr Arg Met Gly
 115 120 125

Asp Asn Cys Ala Ile Pro Ile Thr Val Met Glu Tyr Thr Glu Cys Pro
 130 135 140

Tyr Asn Lys Ser Leu Gly Val Cys Pro Ile Arg Thr Gln Pro Arg Trp
 145 150 155 160

Ser Tyr Tyr Asp Ser Phe Ser Ala Val Ser Glu Asp Asn Leu Gly Phe
 165 170 175

Leu Met His Ala Pro Ala Phe Glu Thr Ala Gly Thr Tyr Leu Arg Leu
 180 185 190

Val Lys Ile Asn Asp Trp Thr Glu Ile Thr Gln Phe Ile Leu Glu His
 195 200 205

Arg Ala Arg Ala Ser Cys Lys Tyr Ala Leu Pro Leu Arg Ile Pro Pro
 210 215 220

Ala Ala Cys Leu Thr Ser Lys Ala Tyr Gln Gln Gly Val Thr Val Asp
 225 230 235 240

Ser Ile Gly Met Leu Pro Arg Phe Ile Pro Glu Asn Gln Arg Thr Val
 245 250 255

Ala Leu Tyr Ser Leu Lys Ile Ala Gly Trp His Gly Pro Lys Pro Pro
 260 265 270

Tyr Thr Ser Thr Leu Leu Pro Pro Glu Leu Ser Asp Thr Thr Asn Ala
 275 280 285

Thr Gln Pro Glu Leu Val Pro Glu Asp Pro Glu Asp Ser Ala Leu Leu
 290 295 300

Glu Asp Pro Ala Gly Thr Val Ser Ser Gln Ile Pro Pro Asn Trp His
305 310 315 320

Ile Pro Ser Ile Gln Asp Val Ala Pro His His Ala Pro Ala Ala Pro
325 330 335

Ser Asn Pro Gly Leu Ile Ile Gly Ala Leu Ala Gly Ser Thr Leu Ala
340 345 350

Val Leu Val Ile Gly Gly Ile Ala Phe Trp Val Arg Arg Arg Ala Gln
355 360 365

Met Ala Pro Lys Arg Leu Arg Leu Pro His Ile Arg Asp Asp Asp Ala
370 375 380

Pro Pro Ser His Gln Pro Leu Phe Tyr
385 390